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UNIVERSITÀ DEGLI STUDI DI TORINO

INFERRING THE INFECTION BIOLOGY OF THE WOOD DECAY FUNGUS *PERENNIPORIA FRAXINEA* THROUGH AN ANALYSIS OF GENOTYPIC DIVERSITY: A CASE STUDY IN NORTHERN ITALY.

F. Sillo[1], L. Giordano[1], D. Astegiano[2], C. Girometta[2], E. Savino[2], A.M. Picco[2], P. Gonthier[1]. *[1]Department of Agricultural, Forest and Food Sciences (DISAFA), University of Torino, Largo Paolo Braccini 2, I-10095 Grugliasco (TO), Italy. [2]Department of Earth and Environmental Sciences (DSTA), University of Pavia, Via S. Epifanio 14, I-27100 Pavia, Italy. E-mail: paolo.gonthier@unito.it*

Perenniporia fraxinea is a fungal pathogen causing wood decay in roots and bole of a wide variety of broadleaf tree species. Despite the crucial role played by *P. fraxinea* in wood decay processes, little is known on how the fungus spreads from tree to tree. In order to clarify its ways of spread, genetic variation among *P. fraxinea* isolates collected from closely located trees was investigated coupling molecular analysis with vegetative incompatibility assays. Twenty samples were isolated from *P. fraxinea* fruiting bodies collected from different standing trees in the Parco della Vernavola (Pavia, Italy) and in several surrounding areas. All the isolates were genotyped by using Random Amplified Microsatellites (RAMS) and somatic incompatibility tests. Analysis through RAMS allowed to distinguish 19 different haplotypes. Somatic incompatibility tests allowed to detect 16 compatibility groups, thus failing to distinguish all haplotypes identified through molecular analysis. These results of genotyping suggest the presence of high intrapopulation diversity, even when isolates collected from closely located trees were compared. These findings may suggest that the spread through root contacts is unlikely for *P. fraxinea*, which rather may spread through basidiospores. In addition, a significant correlation between spatial distribution and genetic variation was observed for the isolates collected in the Parco della Vernavola. This is one of the first genetic population studies on *P. fraxinea* aimed at uncovering its spreading mechanisms.